```
                GenCore version 5.1.7
           Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 12, 2006, 09:12:48 ; Search time 48 Seconds
                                (without alignments)
                     769.917 Million cell updates/sec

Title:     US-10-661-378-9
Perfect score: 2360
Sequence:  1 MEGGWPARQSALLCLTVSLL.........RLYLLFMASSILTVIVLWNT 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:    572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Issued_Patents_AA:*
    1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
    2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
    3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
    4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
    5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
    6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	2360	100.0	447	2	US-09-388-349-9	Sequence 9, Appli
2	717.5	30.4	457	2	US-09-579-250-4	Sequence 4, Appli
3	583.5	24.7	470	2	US-09-579-250-6	Sequence 6, Appli
4	529.5	22.4	441	2	US-09-061-154-2	Sequence 2, Appli
5	526.5	22.3	441	2	US-09-061-154-4	Sequence 4, Appli
6	422.5	17.9	497	1	US-08-278-635B-5	Sequence 5, Appli
7	422.5	17.9	497	2	US-08-464-258B-5	Sequence 5, Appli
8	422.5	17.9	497	2	US-08-471-961-5	Sequence 5, Appli
9	422.5	17.9	497	2	US-09-345-109C-5	Sequence 5, Appli
10	419	17.8	504	2	US-08-660-451A-4	Sequence 4, Appli
11	417.5	17.7	479	1	US-08-278-635B-2	Sequence 2, Appli
12	417.5	17.7	479	2	US-08-464-258B-2	Sequence 2, Appli
13	417.5	17.7	479	2	US-08-471-961-2	Sequence 2, Appli
14	417.5	17.7	479	2	US-09-345-109C-2	Sequence 2, Appli
15	415.5	17.6	494	2	US-08-487-596-10	Sequence 10, Appl
16	415.5	17.6	494	2	US-08-484-722-2	Sequence 2, Appli
17	415.5	17.6	494	2	US-08-660-451A-10	Sequence 10, Appl
18	415.5	17.6	494	2	US-09-703-951A-10	Sequence 10, Appl
19	412.5	17.5	502	2	US-09-579-250-14	Sequence 14, Appli
20	407.5	17.3	502	2	US-09-579-250-10	Sequence 10, Appl
21	405.5	17.2	510	1	US-08-278-635B-4	Sequence 4, Appli
22	405.5	17.2	510	2	US-08-471-961-4	Sequence 4, Appli
23	405.5	17.2	510	2	US-09-345-109C-4	Sequence 4, Appli
24	405	17.2	458	2	US-08-487-596-16	Sequence 16, Appl
25	405	17.2	458	2	US-08-484-722-4	Sequence 4, Appli
26	405	17.2	458	2	US-09-703-951A-16	Sequence 16, Appl
27	404.5	17.1	502	2	US-09-579-250-12	Sequence 12, Appl
28	404.5	17.1	511	2	US-08-464-258B-4	Sequence 4, Appli
29	404	17.1	458	2	US-08-660-451A-16	Sequence 16, Appl
30	404	17.1	458	2	US-09-949-016-5986	Sequence 5986, Ap
31	402.5	17.1	529	1	US-08-496-855A-2	Sequence 2, Appli
32	402.5	17.1	529	2	US-08-487-596-2	Sequence 2, Appli
33	402.5	17.1	529	2	US-08-660-451A-2	Sequence 2, Appli
34	402.5	17.1	529	2	US-09-703-951A-2	Sequence 2, Appli
35	401	17.0	629	2	US-08-278-635B-6	Sequence 6, Appli
36	401	17.0	629	2	US-08-471-961-6	Sequence 6, Appli
37	401	17.0	629	2	US-09-345-109C-6	Sequence 6, Appli
38	400.5	17.0	607	2	US-09-949-016-7817	Sequence 7817, Ap
39	400.5	17.0	627	2	US-08-660-451A-6	Sequence 6, Appli
40	399.5	16.9	502	1	US-08-466-589-8	Sequence 8, Appli
41	399.5	16.9	502	2	US-08-700-636-8	Sequence 8, Appli
42	399.5	16.9	502	2	US-08-467-574-8	Sequence 8, Appli
43	399.5	16.9	502	2	US-09-217-345-8	Sequence 8, Appli
44	399.5	16.9	502	2	US-08-487-596-12	Sequence 12, Appl
45	399.5	16.9	502	2	US-09-892-985-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-388-349-9
; Sequence 9, Application US/0938349
; Patent No. 6365370
; GENERAL INFORMATION:
;  APPLICANT: Dubin, Adreinne B
;  APPLICANT: Erlander, Mark G
;  APPLICANT: Huvar, Arne
;  APPLICANT: Huvar, Rene
;  APPLICANT: Buehler, Lukas K
;  TITLE OF INVENTION: DNA Encoding A Human Subunit 5-HT3-C of the 5-HT3 Serotonin Recept
;  FILE REFERENCE: ORT-1039
;  CURRENT APPLICATION NUMBER: US/09/388,349
;  CURRENT FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;  LENGTH: 447
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-388-349-9

Query Match          100.0%;  Score 2360;  DB 2;  Length 447;
Best Local Similarity 100.0%;  Pred. No. 9.5e-238;
Matches  447;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60
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Db    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60

Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120

Qy  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTF 180

Qy  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMPY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240

Qy  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGYNVFLMMNDLL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGYNVFLMMNDLL 300

Qy  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360
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Qy 361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQLMELWVQFSH 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQLMELWVQFSH 420

Qy 421 AMDTLLFRLYLLFMASSILTVIVLWNT 447
         ||||||||||||||||||||||||||
Db 421 AMDTLLFRLYLLFMASSILTVIVLWNT 447

RESULT 2
US-09-579-250-4
; Sequence 4, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; TITLE OF INVENTION: Conductance
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-579-250-4

  Query Match   30.4%; Score 717.5; DB 2; Length 457;
  Best Local Similarity   35.3%; Pred. No. 4.9e-66;
  Matches 155; Conservative   94; Mismatches 141; Indels   49; Gaps   10;

Qy   51 RKAFRPFTNYSIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPPINWNPKECVGI 110
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Db   20 KKGVRPVRDWRKPTTVSIDVIMYAILNVDEKNQVLTTYIWYRQYWTDEFLQWTPEDFDNV 79

Qy 111 NKLTVLAENLWLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPP 170
         .|| ::.:|:||| |.| :.| : :::|| :||:: |:::: ||||:|.|
Db   80 TKLSIPTDSIWVPDILINEFVDVGKSPNIPYVVHHRGEVQNYKPLQLVTACSLDIYNFP 139

Qy 171 FDQQNCTFTSSFLYTVDSMLLGMDKEVWEITDTSRKVIQTGEWELLGINKATPKMSMG 230
         ||.|| ::|::| | . . : || |: :|.|||||| :. |:
Db 140 FDVQNCSLTFTSWLHTIQDINITLMRSPEEVR-SDKSIFINQGEWELLEVFPQFKEFSID 198

Qy 231 -NNLYDQIMFYVAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGY 289
          .|.| :||||:|||||: | ||||::||:::|:: | ||| |. |:.||||||||
Db 199 ISNSYAEMKFYVIIRRRPLFYAVSLLLPSIFLMVVDIVGFCLPPDSGERVSFKITLLLGY 258

Qy 290 NVFLLMMNDLLPAS-GTPLISVYFALCLSLMVVSLLLETVFITYLLHVATTQPPPMPRWLH 348
         .|||:: .| ||:: ||||| ||| : ::|:::| ||::.|| .: ::.. .:|| :.
Db 259 SVFLIIVSDTLPATIGTPLIGVYFVVCMALLVISLAETIFIPIVRLVHKQDLQ-RPVPDWLR 317

Qy 349 SLLLH------C--TSPGRCCPTAPQKGNK-----------GLGLTLTHLPGPKEPGEL- 388
          :|: | :: | |||||| ||||:|||||
Db 318 HLVLDRIAWILCLGEQPMAHRPPATFQANKTDDCSGSDLLPAMGNHCSHVGGPQDLEKTP 377

Qy 389 --AGKKLGPRETEPDGGSGWTKTQLMEL------------WVQFSHAMDTLLF 427
             | | |:   . :::.| | :::|| ||||::|:|||||
Db 378 RGRGSPLPP---PREASLAVRGLLQELSSIRHFLEKRDEMREVARDWLRVGYVLDRLLF 433

Qy 428 RLYLLFMASSILTVIVLWN 446
         |:||| :.: :| : ||
Db 434 RIYLLAVLAYSITLVTLWS 452

RESULT 3
US-09-579-250-6
; Sequence 6, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent

<hr />

; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; TITLE OF INVENTION: Conductance
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human/mouse
; OTHER INFORMATION: hybrid sequence
US-09-579-250-6

  Query Match   24.7%; Score 583.5; DB 2; Length 470;
  Best Local Similarity   33.2%; Pred. No. 5.2e-52;
  Matches 152; Conservative   73; Mismatches 162; Indels   71; Gaps   15;

Qy   46 QAVFDRKAF----------RPFTNYSIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLV 94
         | .| ||:   :||| |||: :.| ||:|| |.:|: | ||| :|:
Db   22 QGEFQRKLYKELVKNVNPLERPVANDSQPLTVYFSLSLLQIMDVDEKNQVLTTNIWLQMS 81

Qy   95 WDNPPINWNPKECVGINKLTVLAENLWLPDIFIVESMD--VDQTPSGLTAYISSEGRIKY 152
         | : : .||.:   : |:: : .:|:||| :: ::| ||:| ||:|||:|||: |
Db   82 WTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSADERFDAT-FHTNVLVNSSGHCQY 140

Qy 153 DKPMRVTSICNLDIFYFPFDQQNCTFTSSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQ 212
         ::| ..:| :||: :|||| ||| : .: | . || :||| :: :| :
Db 141 LPPGIFKSSCYIDVRWFPFDVQHCKLKFGSWSYGGWSLDLQMQE----ADISGYI--PN 193

Qy 213 GEWELLGI--NKATPKMSMGNNLYDQIMFYVAIRRRPSLYIINLLVPSSFLVAIDALSFY 270
         |||:| || | : . : :||:: || ||||| | ||:||:||:::|:: |
Db 194 GEWDLVGIPGKRSERFYECCKEPYPDVTFTVIIRRRP-FYAVSLLLPSIFLMVVDIVGFC 252

Qy 271 LPAESENRAPFKITLLLGYNVFLLMMNDLLPAS-GTPLISVYFAICLSLMVVSLLLETVFI 329
         || .|. |:.||||||||.|||:: .| ||:: ||||| |||: | :|:::| ||::.|:
Db 253 LPPDSGERVSFKITLLLGYSVFLIIVSDTLPATIGTPLIGVYFVVCMALLVISLAETIFI 312

Qy 330 TYLLHVATTQPPPMPRWLHSLLLH------C--TSPGRCCPTAPQKGNK--------- 370
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Qy 371 GLGLTLTHLPGKPKEPGBL---AGKKLGPRETEPDGGSGWTKTQLMEL---------- 414
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Db 372 AMGNHCSHVGGPQDLEKTPRGRGSPLPP---PREASLAVRGLLQELSSIRHFLEKRDEM 427

Qy 415 ------WVQFSHAMDTLLFRLYLLFMASSILTVIVLWN 446
               ||||::|:|||||:||| :.: :| : ||
Db 428 REVARDWLRVGYVLDRLLFRIYLLAVLAYSITLVTLWS 465

RESULT 4
US-09-061-154-2
; Sequence 2, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```
                GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 12, 2006, 09:05:03 ; Search time 188 Seconds
                                    (without alignments)
                                    1044.693 Million cell updates/sec

Title:         US-10-661-378-9
Perfect score: 2360
Sequence:   1 MEGGWPARQSALLCLTVSLL.........RLYLLFMASSILTVIVLWNT 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:  2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters:    2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  A_Geneseq_21:*
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            4: geneseqp20018:*
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            6: geneseqp20003aa:*
            7: geneseqp20003b8:*
            8: geneseqp20048:*
            9: geneseqp20058:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2360	100.0	447	4	AAB47151	Aab47151 Human 5-H
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3	2348	99.5	447	9	AEC01774	Aec01774 Human 5HT
4	1807.5	76.6	456	6	ABU97389	Abu97389 Human ion
5	1787.5	75.7	471	6	ABU97387	Abu97387 Human ion
6	1787.5	75.7	586	4	AAE10121	Aae10121 Human ion
7	1787.5	75.7	586	6	ABU97383	Abu97383 Human ion
8	1787.5	75.7	586	7	ADE29302	Ade29302 Novel hum
9	1787.5	75.7	614	6	ABU97386	Abu97386 Amino aci
10	1786.5	75.7	471	5	AAU75904	Aau75904 Novel hum
11	1585	67.2	393	4	AAB83413	Aab83413 Human ion
12	1424	60.3	332	4	AAE10122	Aae10122 Human ion
13	1424	60.3	332	6	ABU97382	Abu97382 Amino aci
14	1424	60.3	332	7	ADE29303	Ade29303 Novel hum
15	1036	43.9	267	5	ABP53082	Abp53082 Human TCH
16	996	42.2	192	5	ABP53083	Abp53083 Human TCH
17	975.5	41.3	357	5	AAU75905	Aau75905 Novel hum
18	766	32.5	478	5	ABB08137	Abb08137 Human 5-h
19	766	32.5	478	5	AAU79383	Aau79383 Human 5-h
20	766	32.5	478	7	ADB80480	Adb80480 Ovarian c
21	766	32.5	478	7	ADE62796	Ade62796 Human Pro
22	766	32.5	478	7	ADE61993	Ade61993 Human Pro
23	766	32.5	478	7	ADE62792	Ade62792 Human Pro
24	766	32.5	478	7	ADE56238	Ade56238 Human Pro
25	766	32.5	478	7	ADE61997	Ade61997 Human Pro
26	766	32.5	478	8	ADJ78509	Adj78509 Human 5HT
27	766	32.5	478	8	ADM43151	Adm43151 Human 5HT
28	766	32.5	478	8	ADL82833	Adl82833 Human PRO
29	766	32.5	478	8	ADO05712	Ado05712 Human 5-h
30	766	32.5	478	9	ADX26246	Adx26246 Novel cel
31	766	32.5	519	9	AEC01799	Aec01799 5HT3a wit
32	737.5	31.2	483	9	AEC01773	Aec01773 Human 5HT
33	731.5	31.0	483	7	ADE61991	Ade61991 Rat Prote
34	731.5	31.0	483	7	ADE56236	Ade56236 Rat Prote
35	731.5	31.0	483	7	ADE61995	Ade61995 Rat Prote
36	731.5	31.0	483	8	ADM43149	Adm43149 Rat 5HT3
37	731.5	31.0	483	9	AEC01771	Aec01771 Rat 5HT3.
38	729.5	30.9	477	9	ADX26390	Adx26390 Novel cel
39	729.5	30.9	477	9	AEC01579	Aec01579 Rat 5-hyd
40	727	30.8	483	8	ADJ78510	Adj78510 Mouse 5HT
41	717.5	30.4	457	4	AAB50013	Aab50013 Murine 5H
42	717.5	30.4	487	8	ADM43150	Adm43150 Mouse 5HT
43	717.5	30.4	487	9	ADX26318	Adx26318 Novel cel
44	717.5	30.4	487	9	AEC01772	Aec01772 Mouse 5HT
45	717	30.4	740	8	ADK68027	Adk68027 Yellow fl

ALIGNMENTS

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RESULT 1
AAB47151
ID   AAB47151 standard; protein; 447 AA.
XX
AC   AAB47151;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human 5-HT3-C.
XX
KW   Human; 5-HT3-C; serotonin; 5-HT3-A receptor; nausea; depression; ulcer;
KW   anxiety; psychosis; schizophrenia; urinary continence; anorexia;
KW   Huntington's chorea; tardive dyskinesia; Parkinson's disease; allergy;
KW   obesity; hypertension; migraine; Gilles de la Tourette's syndrome;
KW   sexual dysfunction; drug addiction; Alzheimer's disease; hyperglycemia;
KW   cerebral coma; senile dementia; obsessive-compulsive behavior; asthma;
KW   panic attack; eating disorder; non-insulin dependent diabetes mellitus;
KW   constipation; arrhythmia; stress; inflammation; prostate dysfunction.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 163
FT                  /note= "Encoded by AAA"
FT   Misc-difference 405
FT                  /note= "Encoded by GCA"
XX
PN   WO200116297-A1.
XX
PD   08-MAR-2001.
XX
PF   14-AUG-2000; 2000WO-US022271.
XX
PR   01-SEP-1999;  99US-00388349.
XX
PA   (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
PI   Dubin AE,  Erlander MG,  Huvar A,  Huvar R,  Buehler LK;
XX
PN   WPI; 2001-244402/25.
DR   N-PSDB; AAC85574.
XX
PT   New DNA molecule encoding human 5-HT3-C protein for modifying the
PT   function of a serotonin 5-HT3-A receptor.
XX
PS   Claim 11; Fig 3; 78pp; English.
XX
```

```
CC   This sequence represents human 5-HT3-C protein which may function as a
CC   subunit to modify the function of a serotonin 5-HT3-A receptor.
CC   Recombinant 5-HT3-C is useful for identifying modulators of the 5-HT3
CC   complex and a modulator of human 5-HT3-C subunit activity is useful in
CC   treating conditions that are mediated by 5-HT3-C, for example nausea,
CC   depression, anxiety, psychoses (e.g. schizophrenia), urinary continence,
CC   Huntington's chorea, tardive dyskinesia, Parkinson's disease, obesity,
CC   hypertension, migraine, Gilles de la Tourette's syndrome, sexual
CC   dysfunction, drug addiction/abuse, cognitive disorders, Alzheimer's
CC   disease, cerebral coma, senile dementia, obsessive-compulsive behavior,
CC   panic attacks, pain, social phobias, eating disorder and anorexia,
CC   cardiovascular and cerebrovascular disorders, non-insulin dependent
CC   diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of
CC   the neuroendocrine system, stress and spasticity as well as ulcers,
CC   airway constriction, asthma, allergy, inflammation and prostate
CC   dysfunction
XX
SQ   Sequence 447 AA;

Query Match            100.0%;  Score 2360;  DB 4;  Length 447;
Best Local Similarity  100.0%;  Pred. No. 1.6e-225;
Matches  447;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60

Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120

Qy  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPPFDQQNCTFTF 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPPFDQQNCTFTF 180

Qy  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240

Qy  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLGYNVFLLMMNDLL 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLGYNVFLLMMNDLL 300

Qy  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPMPRWLHSLLLHCTSPGRC 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPMPRWLHSLLLHCTSPGRC 360

Qy  361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQLMELWVQFSH 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQLMELWVQFSH 420

Qy  421 AMDTLLFRLYLLFMASSIITVIVLWNT 447
         ||||||||||||||||||||||||||
Db  421 AMDTLLFRLYLLFMASSIITVIVLWNT 447

RESULT 2
ADM43152
ID   ADM43152 standard; protein; 447 AA.
XX
AC   ADM43152;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human 5HT3C subunit.
XX
KW   human; INPIONCH1; serotonin receptor; antiemetic; analgesic;
KW   antialcoholic; neuroleptic; antiinflammatory; gastrointestinal;
KW   neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
KW   tranquiliser; antidepressant; antiasthmatic; endocrine; cardiovascular;
KW   antipsoriatic; antirheumatic; antiarthritic; haemostatic; antidiabetic;
KW   dermatological; ophthalmological; cytostatic; anti-HIV; virucide;
KW   antibacterial; antitubercular; tuberculostatic; fungicide; gene therapy;
```

```
KW   vaccine; 5-HT3 receptor; 5HT3C.
XX
OS   Homo sapiens.
XX
PN   WO2004009633-A1.
XX
PD   29-JAN-2004.
XX
PF   21-JUL-2003; 2003WO-GB003130.
XX
PR   19-JUL-2002; 2002GB-00016903.
XX
PA   (INPH-) INPHARMATICA LTD.
XX
PI   Lobley AE, Michalovich D, Stancovski I, Allen KE, Allen JM,
PI   Osypenko VN, Gurney AM;
XX
DR   WPI; 2004-123379/12.
XX
PT   New INPIONCH1 polypeptides having serotonin receptor activity, useful for
PT   diagnosing, preventing or treating diseases such as cancer, Alzheimer's
PT   disease, inflammation, HIV, sexual dysfunction or cardiovascular
PT   disorders.
XX
PS   Disclosure; Fig 4; 106pp; English.
XX
CC   The invention relates to novel INPIONCH1 polypeptides having serotonin
CC   receptor activity. A polypeptide of the invention has antiemetic,
CC   analgesic, antialcoholic, neuroleptic, antiinflammatory, gastrointestinal
CC   -gen., neuroprotective, nootropic, antiparkinsonian, anticonvulsant,
CC   tranquiliser, antidepressant, antiasthmatic, endocrine-gen.,
CC   cardiovascular-gen., antipsoriatic, antirheumatic, antiarthritic,
CC   haemostatic, antidiabetic, dermatological, ophthalmological, cytostatic,
CC   anti-HIV, virucide, antibacterial, antitubercular, tuberculostatic, and
CC   fungicide activity, and may have a use in gene therapy, or a vaccine. The
CC   polypeptide, nucleic acid molecule, vector, host cell, ligand or compound
CC   is useful in the therapy or diagnosis of diseases. These may also be used
CC   in the manufacture of a medicament for the treatment of diseases
CC   including, but not limited to, nausea, vomiting, pain, eating disorders,
CC   alcoholism, psychosis, side effects of various anticancer therapies,
CC   irritable bowel syndrome, gastrointestinal-related disorders, Alzheimer's
CC   disease, Parkinson's disease, Huntington's Chorea, cognitive disorders,
CC   behavioural disorders and phobias such as anxiety related illnesses and
CC   addiction, obsessive-compulsive behaviour, memory and learning disorders,
CC   depression and panic disorders, asthma, inflammation, sexual dysfunction,
CC   disorders of the neuroendocrine and cardiovascular systems, or diseases
CC   associated with T-cells such as inflammatory bowel diseases (including
CC   Crohn's disease and ulcerative colitis), multiple sclerosis, psoriasis,
CC   rheumatoid arthritis, thrombocytopenia, type I diabetes mellitus, atopic
CC   dermatitis, atopic rhinitis and conjunctivitis, diseases associated with
CC   T-cell proliferation such as leukaemias, diseases associated with T-cell
CC   depletion such as HIV infection, chemotherapy and radiotherapy, and
CC   diseases where regulation of T-cell activation is required, such as
CC   cancers, viral infections, bacterial infections (including tuberculosis)
CC   and fungal infections. The polypeptide is also used as a member of the 5-
CC   HT3 receptor group. The present sequence is used in the exemplification
CC   of the invention.
XX
SQ   Sequence 447 AA;

Query Match            99.5%;  Score 2348;  DB 8;  Length 447;
Best Local Similarity  99.6%;  Pred. No. 2.4e-224;
Matches  445;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60

Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120

Qy  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPPFDQQNCTFTF 180
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:      April 12, 2006, 09:08:53 ; Search time 40 Seconds
                                        (without alignments)
                                        1075.222 Million cell updates/sec

Title:       US-10-661-378-9
Perfect score: 2360
Sequence:    1 MEGGWPARQSALLCLTVSLL..........RLYLLFMASSILTVIVLWNT 447
Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
             1: pir1:*
             2: pir2:*
             3: pir3:*
             4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	722	30.6	462	2	I58179	5HT3 receptor subu
2	717	30.4	489	2	S41757	5-hydroxytryptamin
3	446.5	18.9	464	2	A33523	nicotinic acetylch
4	435	18.4	528	1	ACCH2N	nicotinic acetylch
5	426	18.1	495	2	S60589	acetylcholine rece
6	422	17.9	499	2	A24572	nicotinic acetylch
7	419	17.8	503	2	A53956	nicotinic acetylch
8	417.5	17.7	479	2	A55382	nicotinic acetylch
9	417	17.7	494	2	T09289	nicotinic acetylch
10	414	17.5	455	2	A55972	nicotinic acetylch
11	408	17.3	502	2	A37040	nicotinic acetylch
12	407	17.2	512	2	B37014	nicotinic acetylch
13	406.5	17.2	622	1	ACCH4N	nicotinic acetylch
14	404.5	17.1	511	2	A40110	nicotinic acetylch
15	403	17.1	423	2	I38056	nicotinic acetylch
16	401	17.0	455	2	S51116	nicotinic acetylch
17	400.5	17.0	462	2	S06893	nicotinic acetylch
18	400.5	17.0	627	2	JC4021	nicotinic acetylch
19	399.5	16.9	502	1	ACHUA7	nicotinic acetylch
20	398.5	16.9	501	2	A25338	nicotinic acetylch
21	397.5	16.8	502	2	JN0113	nicotinic acetylch
22	397	16.8	625	2	A26456	nicotinic acetylch
23	395.5	16.8	505	2	S07227	nicotinic acetylch
24	394	16.7	466	2	S16333	nicotinic acetylch
25	393.5	16.7	502	2	G02259	alpha 7 neuronal n
26	392.5	16.6	502	2	A57175	nicotinic acetylch
27	392.5	16.6	502	2	T01378	nicotinic receptor
28	391	16.6	502	2	S10505	nicotinic acetylch
29	389.5	16.5	454	2	B39218	nicotinic acetylch

30	387	16.4	576	1	ACFFA2	nicotinic acetylch
31	386.5	16.4	491	1	ACCHNN	nicotinic acetylch
32	385.5	16.3	501	2	S04607	nicotinic acetylch
33	385	16.3	511	2	JH0173	alpha-bungarotoxin
34	384.5	16.3	560	2	T19622	hypothetical prote
35	383.5	16.2	459	2	S14703	nicotinic acetylch
36	381	16.1	513	2	ACCHD1	nicotinic acetylch
37	380.5	16.1	452	2	A35721	probable nicotinic
38	380	16.1	517	2	A30992	nicotinic acetylch
39	379	16.1	517	2	S13875	nicotinic acetylch
40	378.5	16.0	501	2	S13873	nicotinic acetylch
41	376	15.9	470	2	A39218	nicotinic acetylch
42	376	15.9	503	2	JH0174	nicotinic acetylch
43	375	15.9	520	1	ACMSD1	nicotinic acetylch
44	373	15.8	521	2	C28529	nicotinic acetylch
45	371.5	15.7	498	2	G02421	nicotinic acetylch

```
                          ALIGNMENTS

RESULT 1
I58179
5HT3 receptor subunit - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58179
R;Isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Yang
Neuroreport 5, 121-124, 1993
A;Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit.
A;Reference number: I58179; MUID:9154206; PMID:7509203
A;Accession: I58179
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-462 <RES>
A;Cross-references: UNIPARC:UPI0000170C0B; EMBL:U01227; NID:g402245; PIDN:AAA52182.1; PII
C;Superfamily: acetylcholine receptor

Query Match       30.6%;    Score 722;   DB 2;   Length 462;
Best Local Similarity  35.5%;   Pred. No. 4.7e-51;
Matches 153;  Conservative  96; Mismatches 144;  Indels  38;  Gaps    9;

Qy   51 RKAFRPFTNYSIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGI 110
            ||: ::|: |: |:||||| ::::|| :||:::::|||:::|| ||:|:::||:::::|
Db   30 KKGVRFVRDWRKPTLVSIDVIMYAILNVDBKNQVLTYIWTRQFWTDBFLQWTBDFDNV 89

Qy  111 NKLTVLAENLWLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFP 170
         :|||:||||:|||: |:::::||||||:| :||:::::||||||||:|||||||||||||
Db   90 TKLSIPTDSIWVPDILLNEFVDVGKSPSIPYVYVHHQGEVQNYKPLQLVTACSLDIYNFP 149

Qy  171 FDQQNCTFTFSSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSM- 229
            ||||||: :||: :|:|: :||||:|:|:: :: :::: |||||||||
Db  150 FDVQNCSLTFTSWLHTIQDINISLWRTPEEVR-SDKSIFINQGEWELLGVFTKFQEFSIE 208

Qy  230 GNNLYDQIMFYVAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGY 289
            :: ::| :||||||:|||||||||||||:: |:||:||:::||||::|||:||||||||
Db  209 TSNSYAEMKFVVIRRRPLFYAVSLLLPSIFLMVVDIVGFCLPPDSGBRVSFKITLLLGY 268

Qy  290 NVFLLMWNDLLPASG--TPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWL 347
            :|||||||||||:||  ||||||| :||||||||||:|::|:|||||||||||||||
Db  269 SVFLIIVSDTLPATAIRTPLIGVYFVVCMALLVISLAETIFIVQLVHKQDLQ-RPVPDWL 327

Qy  348 HSLLLH------C--TSPGRCCPTAPQKGNK---GLGLTLHLPGKPEPGELAGKKLG 394
            :|:|        |:|
Db  328 RHLVLDRIAWLLCLGEQPMAHRPPATFQANKTDDCSAMGNHCSHVGSPQDLEKTSRSRDS 387

Qy  395 PRETBPDGGSGWTKTQLMEL----------------------WVQFSHAMDTLLFRLYLLFMA 435
            |||||                |::||:||||||||:|||
Db  388 PL-PPPREASLAVRGLLQELSSIRHSLEKRDEMREVARDWLRVGYVLDRLLFRIYLLAVL 446

Qy  436 SSILTVIVLWN 446
           ::|:|:||:
Db  447 AYSITLVTLWS 457
```

RESULT 2
S41757
5-hydroxytryptamine-3 receptor - mouse
N;Alternate names: serotonin-gated ion channel 5HT3
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S41757; S43205; S48111; S45019; S45020; A40832; I48229; I48230
R;Uetz, P.; Abdelatty, F.; Villarroel, A.; Rappold, G.; Weiss, B.; Koenen, M.
A;Title: Organisation of the murine 5-HT(3) receptor gene and assignment to human chromo
FEBS Lett. 339, 302-306, 1994
A;Reference number: S41757; MUID:94156052; PMID:8112471
A;Accession: S41757
A;Molecule type: DNA
A;Residues: 1-489 <UET1>
A;Cross-references: UNIPARC:UPI00001779AA; EMBL:Z22772
R;Uetz, P.
A;Note: the authors translated the codon TAC for residue 142 as His, GTG for residue 143
submitted to the EMBL Data Library, May 1993
A;Reference number: S43205
A;Accession: S43205
A;Molecule type: DNA
A;Residues: 1-30,'E',33-303,305-311,'I',313-385,'T',387-489 <UET2>
A;Cross-references: UNIPARC:UPI00001779AB; EMBL:Z22772
R;Hope, A.G.; Downie, D.L.; Sutherland, L.; Lambert, J.J.; Peters, J.A.; Burchell, B.
Eur. J. Pharmacol. 245, 187-192, 1993
A;Title: Cloning and functional expression of an apparent splice variant of the murine 5
A;Reference number: S48111; MUID:93259238; PMID:7683998
A;Accession: S48111
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-74,'V',76-384,391-489 <HOP>
A;Cross-references: UNIPARC:UPI00001779CB99; EMBL:X72395; NID:g313863; PIDN:CAA51089.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R;Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundstrvm, K.; Buell, G.; Humbert, Y.;
submitted to the EMBL Data Library, May 1994
A;Description: Organization of the mouse 5HT3 receptor gene and functinoal expression of
A;Reference number: S45019
A;Accession: S45019
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7,'G',8-30,'E',33-303,305-489 <MAR>
A;Cross-references: UNIPARC:UPI00001779AC; GB:M74425
R;Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundstrom, K.; Buell, G.; Humbert, Y.;
Brain Res. Mol. Brain Res. 26, 233-241, 1994
A;Title: Organization of the mouse 5-HT3 receptor gene and functional expression of two
A;Reference number: I48229; MUID:95157178; PMID:7854052
A;Accession: I48229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-384,391-394,'T',396-489 <RES>
A;Cross-references: UNIPARC:UPI00001779CB9B; EMBL:X79283; NID:g488693; PIDN:CAA55871.1; PI
A;Accession: I48230
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-394,'T',396-489 <RE2>
A;Cross-references: UNIPARC:UPI00001779CB9A; EMBL:X79283; NID:g488693; PIDN:CAA55870.1; PI
C;Genetics:

A;Introns: 23/1; 78/3; 93/3; 130/2; 187/1; 240/3; 311/1; 385/1
C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane r
F;247-273/Domain: transmembrane #status predicted <TM1>
F;279-297/Domain: transmembrane #status predicted <TM2>
F;308-326/Domain: transmembrane #status predicted <TM3>
F;467-486/Domain: transmembrane #status predicted <TM4>

Query Match   30.4%;   Score 717;   DB 2;   Length 489;
Best Local Similarity 35.2%;   Pred. No. 1.3e-50;
Matches 155;   Conservative   94;   Mismatches 141;   Indels 50;   Gaps 10;

Qy   51 RKAFRPFTNYSIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLIVWDNPFINWNPKECVGI 110
             ||::| :||: :|||||::|: ||| || ::: |||::|: ::|::|
Db   51 KKGVRPVRDWRKPTTVSIDVIMYAILNVDEKNQVLTTYIWYRQYWTDEFLQWTPEDFDNV 110

Qy   111 NKLTVLAENLWLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFP 170
             ||||:| :: ::|: ::| | || || : |||| | |:| |||||||||||||
Db   111 TKLSIPTDSIWPDLILINEFVDVGKSPNIPVVYVHHRGEVQNYKPLQLVTACSLDIYNFP 170

Qy   171 FDQQNCTFTFSSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMG 230
             || ::|::|:|:|:|:||:| ||: : |||:::|||| | ||::|
Db   171 FDVQNCSLITFTSWLHTIQDINITLWRSPEEVR-SDKSIFNQGEWELLEVFPQFKEFSID 229

Qy   231 -NNLYDQIMFYVAIRRRPSLYIINLLVPSSFIVAIDALSFYLPAESENRAPPKITLLGY 289
             :|| :|||::|||||||::|||| :::|||::|||:|:|||::| : ||| |||
Db   230 ISNSYAEMKFYVIIRRRPLFYAVSLLLPSIFLMVVDIVGFCLPPDSGERVSFKITLLGY 289

Qy   290 NVFLMMNDLLPAS--GTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPMPRWL 347
             || |: |:|:| ||:||| |::::||::|::|||:|:::||:||| |::||:|
Db   290 SVFLIIVSDTLPATAIGTPLIGVYFVVCMALLVISLAETIFIVRLVHKQDLQ-RPVPDWL 348

Qy   348 HSLLLH------C-TSPGRCCPTAPQKGNK----------------GLGLTLTHLPGPKEPGEL 388
             |:|: |::: :::   :|::||
Db   349 RHLVLDRIAWILCLGEQPMAHRPPATFQANKTDDCSGGSDLLPAMGNHCSHVGGPQDLEKT 408

Qy   389 --AGKKLGPRETBPDGGSGWTKTQLMEL---------------WVQFSHAMDTLIL 426
             || | ||: ::: :||
Db   409 PGRGSPLPP---PREASLAVRGLLQELSSIRHFLEKRDEMREVARDWLRVGVVLDRLL 464

Qy   427 FRLYLLFMASSILTVLVLWN 446
             |::|||::|::|||:|:
Db   465 FRIYLLAVLAYSITLVTLWS 484

RESULT 3
A33523
nicotinic acetylcholine receptor beta-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 09-Jul-2004
C;Accession: A33523
R;Deneris, E.S.; Boulter, J.; Swanson, L.W.; Patrick, J.; Heinemann, S.
J. Biol. Chem. 264, 6268-6272, 1989
A;Title: Beta-3: a new member of nicotinic acetylcholine receptor gene family is expresse
A;Reference number: A33523; MUID:89197926; PMID:2703489
A;Accession: A33523
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-464 <DEN>
A;Cross-references: UNIPROT:P12391; UNIPARC:UPI0000125273; GB:J04636; NID:g3298521; PIDN:
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match   18.9%;   Score 446.5;   DB 2;   Length 464;
Best Local Similarity 27.3%;   Pred. No. 1.3e-28;
Matches 127;   Conservative   86;   Mismatches 196;   Indels 57;   Gaps 14;

Qy   15 LTVSLLLQGRGDAFTINC--SGFDQHGVGDPAVFQAVFD--RKAFRPFTNYSIPTRVNISF 70
             |::|: || | :| |: :|: : || : : |||||||||::||| ::||
Db   9 LVLSATLSGSWVTLTATAGLSSVAEH--EDALLRHLFQGYQKWVRPVLNSSDIIKVYFGL 66

Qy   71 TLSAILGVDAQLQLLTSFLWMDLIVWDNPFINWNPKECVGINKLTVLAENLWLPDIFIVES 130
             || ::| : ||: || | |: || ::||:|::|:

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                  GenCore version 5.1.7
           Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 12, 2006, 09:24:04 ; Search time 167 Seconds
                                       (without alignments)
                                       1118.381 Million cell updates/sec

Title:         US-10-661-378-9
Perfect score: 2360
Sequence:      1 MEGGWPARQSALLCLTVSLL.........RLYLLFMASSILTVIVLWNT 447

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:    1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published Applications AA_Main:*
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              2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
              3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
              4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
              5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
              6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
```

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2360	100.0	447	3	US-09-955-524-9	Sequence 9, Appli
2	2360	100.0	447	4	US-10-661-378-9	Sequence 9, Appli
3	1795	76.1	457	4	US-10-243-475-132	Sequence 132, App
4	1787.5	75.7	471	4	US-10-243-475-121	Sequence 121, App
5	1787.5	75.7	586	5	US-09-802-668-105	Sequence 105, App
6	1787.5	75.7	586	4	US-10-243-475-105	Sequence 105, App
7	1787.5	75.7	614	4	US-09-495-495-119	Sequence 119, App
8	1786.5	75.7	471	3	US-09-899-495-116	Sequence 116, App
9	1585	67.2	393	4	US-10-149-930-50	Sequence 50, Appl
10	1424	60.3	332	3	US-09-802-668-106	Sequence 106, App
11	1424	60.3	332	4	US-10-243-475-106	Sequence 106, App
12	975.5	41.3	357	3	US-09-899-495-118	Sequence 118, App
13	766	32.5	478	4	US-10-173-999-44	Sequence 44, Appl
14	766	32.5	478	4	US-10-399-405-3	Sequence 3, Appli
15	766	32.5	478	5	US-10-684-206-12	Sequence 12, Appli
16	766	32.5	478	5	US-10-756-149-5336	Sequence 5336, Ap
17	729.5	30.9	477	5	US-10-973-858-12	Sequence 12, Appli
18	717.5	30.4	457	4	US-10-740-083-4	Sequence 4, Appli
19	583.5	24.7	470	4	US-10-740-083-6	Sequence 6, Appli
20	420	17.8	450	3	US-09-795-693-11	Sequence 11, Appli
21	420	17.8	450	4	US-10-156-239-11	Sequence 11, Appl
22	420	17.8	450	4	US-10-199-485-11	Sequence 11, Appl
23	420	17.8	450	4	US-10-312-088-38	Sequence 38, Appl
24	420	17.8	450	5	US-10-343-903-15	Sequence 15, Appl
25	420	17.8	450	5	US-10-687-268-38	Sequence 38, Appl
26	419	17.8	504	4	US-10-349-836-4	Sequence 4, Appli
27	419	17.8	504	5	US-10-723-860-3689	Sequence 3689, Ap
28	415.5	17.6	494	4	US-10-349-836-10	Sequence 10, Appl
29	415.5	17.6	494	4	US-10-303-198-2	Sequence 2, Appl
30	413	17.5	499	5	US-10-769-085-13	Sequence 13, Appl
31	412.5	17.5	502	4	US-10-740-083-14	Sequence 14, Appl
32	408	17.3	502	4	US-10-157-031-92	Sequence 92, Appl
33	408	17.3	631	3	US-09-941-179A-7	Sequence 7, Appli
34	407.5	17.3	502	4	US-10-740-083-10	Sequence 10, Appl
35	404.5	17.1	502	4	US-10-740-083-12	Sequence 12, Appl
36	404	17.1	458	4	US-10-349-836-16	Sequence 16, Appl
37	404	17.1	458	4	US-10-303-198-4	Sequence 4, Appli
38	402.5	17.1	502	5	US-10-769-085-11	Sequence 11, Appl
39	402.5	17.1	529	4	US-10-349-836-2	Sequence 2, Appli
40	402.5	17.1	529	4	US-10-415-014-702	Sequence 702, App
41	402.5	17.1	529	4	US-10-415-014-704	Sequence 704, App
42	402.5	17.1	529	4	US-10-415-014-705	Sequence 705, App
43	402.5	17.1	529	4	US-10-757-262-86	Sequence 86, Appl
44	402.5	17.1	529	5	US-10-643-795A-112	Sequence 112, App
45	402.5	17.1	529	5	US-10-643-795A-121	Sequence 121, App

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                         ALIGNMENTS

RESULT 1
US-09-955-524-9
; Sequence 9, Application US/0995524
; Patent No. US2002013713BA1
; GENERAL INFORMATION:
;  APPLICANT: Dubin, Adrienne E
;  APPLICANT: Erlander, Mark G
;  APPLICANT: Huvar, Arne
;  APPLICANT: Huvar, Rene
;  APPLICANT: Buehler, Lukas K
;  TITLE OF INVENTION: DNA ENCODING A HUMAN SUBUNIT 5-HT3-C OF THE 5-HT3 SEROTONIN
;  TITLE OF INVENTION:  RECEPTOR
;  FILE REFERENCE: ORT-1039
;  CURRENT APPLICATION NUMBER: US/09/955,524
;  CURRENT FILING DATE: 2001-09-15
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 9
;  LENGTH: 447
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-955-524-9

  Query Match             100.0%;  Score 2360;  DB 3;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-213;
  Matches  447;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
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Qy  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTIF 180
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Db  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTIF 180

Qy  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240
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Qy  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLGYNVFLLMMNDLL 300
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Db  241 VAIRRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLGYNVFLLMMNDLL 300

Qy  301 PASGTPLISVFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360
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Db  301 PASGTPLISVFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360
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Qy    421  AMDTLLFRLYLLFMASSILTVIVLWNT 447
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RESULT 2
US-10-661-378-9
; Sequence 9, Application US/10661378
; Publication No. US2005124795A1
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Huvar, Arne
; APPLICANT: Huvar, Rene
; APPLICANT: Buehler, Lukas K
; TITLE OF INVENTION: DNA ENCODING A HUMAN SUBUNIT 5-HT3-C OF THE 5-HT3 SEROTONIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: ORT-1039
; CURRENT APPLICATION NUMBER: US/10/661,378
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/955,524
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-378-9

Query Match   100.0%; Score 2350; DB 5; Length 447;
Best Local Similarity   100.0%; Pred. No. 1.9e-213;
Matches 447; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
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Qy   181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240
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RESULT 3
US-10-243-475-132
; Sequence 132, Application US/10243475
; Publication No. US20030194720A1
; GENERAL INFORMATION:
;  APPLICANT: Roberds, Steven L.
;  APPLICANT: Benjamin, Christopher W.
;  APPLICANT: Karnovsky, Alla M.
;  APPLICANT: Ruble, Cara L.
;  TITLE OF INVENTION: Human Ion Channels
;  FILE REFERENCE: PHRM0039-100
;  CURRENT APPLICATION NUMBER: US/10/243,475
;  CURRENT FILING DATE: 2003-01-16
;  PRIOR APPLICATION NUMBER: 60/403,254
;  PRIOR FILING DATE: 2002-08-13
;  PRIOR APPLICATION NUMBER: 60/318,733
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
;  LENGTH: 457
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-243-475-132

Query Match             76.1%;  Score 1795;  DB 4;  Length 457;
Best Local Similarity   73.5%;  Pred. No. 3.8e-160;
Matches  336;  Conservative  44;  Mismatches  67;  Indels  10;  Gaps   2;

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Qy     60  YSIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAEN 119
           :|.:||||  || || : |||::||| ::|:| ||  :|:::|:||:|   || :::::|
Db     61  ISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPECEGITKMSMAAKN 120

Qy    120  LWLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPPFDQQNCTFT 179
           ||||||||||:|||||||| ||||||::||| |:|:|:|  |  |:|||:|||:|||||
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Db    181  FSSFLYTVDSMLLDMEKEVWEITDASRNILQTHGEWELLGLSKATAKLSRGNLYDQIVF 240

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           |||||||||||||:|||||| |||||||||||:|::   | || |||| ||:||:| :|
Db    241  YVAIRRRPSLYIVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLLGYNVFLIMSDL 300

Qy    300  LPASGTPLISVYFALCLSLMVVSLLETVFITYLLLHVATTQPPMPRWLHSLLLHCTSPGR 359
           ||||:|||||:||| |||||||||||| :||||||:|||||:|||:|:||||:|||||:
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Db    421  SVELWLQFSHAMDAMLFRLYLLFMASSIITVICLWNT 457
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RESULT 4
US-10-243-475-121
; Sequence 121, Application US/10243475
; Publication No. US20030194720A1
; GENERAL INFORMATION:
; APPLICANT: Roberds, Steven L.
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: PHRM0039-100
; CURRENT APPLICATION NUMBER: US/10/243,475

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                 GenCore version 5.1.7
         Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run qn:    April 12, 2006, 09:25:03 ; Search time 27 Seconds
                                       (without alignments)
                                       703.433 Million cell updates/sec

Title:           US-10-661-378-9
Perfect score:   2360
Sequence:        1 MEGGWPARQSALLCLTVSLL.........RLYLLFMASSLTVIVLWNT 447

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters:   217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA New:*
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        2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
        3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
        4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
        5: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
        6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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2	727	30.8	483	7	US-11-037-829A-5	Sequence 5, Appli
3	529	22.4	495	7	US-11-037-829A-7	Sequence 7, Appli
4	415.5	17.6	494	7	US-11-122-144-10	Sequence 10, Appl
5	405	17.2	458	7	US-11-122-144-16	Sequence 16, Appl
6	402.5	17.1	529	7	US-11-122-144-2	Sequence 2, Appli
7	400.5	17.0	627	7	US-11-037-829A-1	Sequence 1, Appli
8	399.5	16.9	502	7	US-11-122-144-12	Sequence 12, Appli
9	399.5	16.9	627	7	US-11-122-144-6	Sequence 6, Appli
10	398	16.9	491	7	US-11-037-829A-9	Sequence 9, Appli
11	391	16.6	502	7	US-11-122-144-14	Sequence 14, Appl
12	388	16.4	502	7	US-11-037-829A-2	Sequence 2, Appli
13	373.5	15.8	485	7	US-11-037-829A-11	Sequence 11, Appl
14	372	15.8	504	7	US-11-122-144-4	Sequence 4, Appli
15	371.5	15.7	498	7	US-11-037-829A-3	Sequence 3, Appli
16	371.5	15.7	498	7	US-11-122-144-18	Sequence 18, Appl
17	360	15.3	468	7	US-11-122-144-8	Sequence 8, Appli
18	250.5	10.6	481	6	US-10-512-376-5	Sequence 5, Appli
19	245.5	10.4	459	6	US-10-512-376-6	Sequence 6, Appli
20	239	10.1	467	6	US-10-512-376-3	Sequence 3, Appli
21	239	10.1	496	6	US-10-512-376-2	Sequence 2, Appli
22	229	9.7	487	7	US-11-241-631-13	Sequence 13, Appl
23	229	9.0	475	7	US-11-241-631-16	Sequence 16, Appl
24	213	9.0	487	7	US-11-241-631-14	Sequence 14, Appl
25	213	9.0	506	7	US-11-241-631-15	Sequence 15, Appl
26	192.5	8.2	497	7	US-11-037-829A-15	Sequence 15, Appl
27	190	8.1	448	7	US-11-241-631-17	Sequence 17, Appl
28	181	7.7	474	7	US-11-037-829A-13	Sequence 13, Appl
29	180.5	7.6	473	7	US-11-169-041-229	Sequence 229, App
30	180	7.6	492	7	US-11-037-829A-12	Sequence 12, Appl
31	177	7.5	485	6	US-10-204-029-7	Sequence 7, Appli
32	169.5	7.2	345	7	US-11-188-353-10	Sequence 10, Appl
33	169.5	7.2	392	7	US-11-188-353-4	Sequence 4, Appli
34	169.5	7.2	420	7	US-11-188-353-8	Sequence 8, Appli
35	169.5	7.2	467	7	US-11-188-353-2	Sequence 2, Appli
36	167	7.1	226	6	US-10-512-376-8	Sequence 8, Appli
37	164	6.9	465	7	US-11-037-829A-14	Sequence 14, Appl
38	160	6.8	422	6	US-10-204-029-4	Sequence 4, Appli
39	160	6.8	426	6	US-10-204-029-2	Sequence 2, Appli
40	98.5	4.2	626	7	US-11-188-298-2725	Sequence 2725, Ap
41	97.5	4.1	264	7	US-11-241-631-18	Sequence 18, Appl
42	95.5	4.0	574	6	US-10-518-341-1	Sequence 1, Appli
43	95.5	4.0	574	7	US-11-022-562-214	Sequence 214, App
44	94	4.0	559	7	US-11-087-099-6637	Sequence 6637, Ap
45	94	4.0	559	7	US-11-188-298-17098	Sequence 17098, A

ALIGNMENTS

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RESULT 1
US-11-037-829A-4
; Sequence 4, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
;       APPLICANT: Targacept, Inc
;       APPLICANT: Catholic Healthcare West
;       APPLICANT: Bencherif, Merouane
;       APPLICANT: Lukas, Ronald J.
;       TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
;       TITLE OF INVENTION: Nicotinic Receptor Subunits
;       FILE REFERENCE: T103 1520.PCT
;       CURRENT APPLICATION NUMBER: US/11/037,829A
;       CURRENT FILING DATE: 2005-01-18
;       PRIOR APPLICATION NUMBER: US 60/397,380
;       PRIOR FILING DATE: 2002-07-19
;       NUMBER OF SEQ ID NOS: 15
;       SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;       LENGTH: 478
;       TYPE: PRT
;       ORGANISM: Homo sapien
US-11-037-829A-4

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  Matches  175;  Conservative   94;  Mismatches  151;  Indels   66;  Gaps   14;

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Db      6 QQALLALLPTLL-AQGEARR------SRNTTRPALLR-LSDYLLTNYRKGVRPVRDWRK 57

Qy     63 PTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENLWL 122
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Qy    123 PDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYPPPDQQNCTFTFSS 182
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Qy    183 FLYTVDSMLLGMDKEVWEITD--TSRKVIQTGEWELLGINKATPKMSM-GNNLYDQIM 238
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Qy    239 FYVAIRRRPSLYIINLLVPSSFLVAIDALSFYLPASSENRAPPKITLLGYNVFLLMMND 298
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Qy 299 LLPAS--GTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTS 356
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Qy   357 PGRCC-------PTAPQKGNK-----GLGLTLTHLPGP---KEPGELAGKKLGPRETE 399
Db   353 WLLCLREQSTSQRPPATSQATKTDDCSAMGNHCSHMGGPQDFEKSPRDRCSPPPPPRE-- 410

Qy   400 PDGGSGWTKTQLMEL----------------WVQFSHAMDTLFLFRYLLFMASSILT 440
Db   411 ---ASLAVCGLLQELSSIRQFLEKRDEIREVARDWLRVGSVLDKLLFHIYLLAVLAYSIT 467

Qy   441 VIVLWN 446
Db   468 LVMLWS 473

RESULT 2
US-11-037-829A-5
; Sequence 5, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
;   APPLICANT: Targacept, Inc
;   APPLICANT: Catholic Healthcare West
;   APPLICANT: Bencherif, Merouane
;   APPLICANT: Lukas, Ronald J.
;   TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
;   TITLE OF INVENTION: Nicotinic Receptor Subunits
;   FILE REFERENCE: T103 1520.PCT
;   CURRENT APPLICATION NUMBER: US/11/037,829A
;   CURRENT FILING DATE: 2005-01-18
;   PRIOR APPLICATION NUMBER: US 60/397,380
;   PRIOR FILING DATE: 2002-07-19
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 483
;   TYPE: PRT
;   ORGANISM: Mouse
US-11-037-829A-5

Query Match   30.8%; Score 727; DB 7; Length 483;
Best Local Similarity   35.9%; Pred. No. 3.2e-61;
Matches 156; Conservative 94; Mismatches 140; Indels 44; Gaps 10;

Qy   51 RKAFRPFTNSYSIPTRVNISFTLSAILGVDAQLQLLTSFLMDLVWDNPFINWNPKECVGI 110
Db   51 KKGVRPVRDWRKPTTVSIDVIMYAILNVDEKNQVLTTVIWYRQVTWTDEFLQWTPEDFDNV 110

Qy   111 NKLTVLAENLWLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFP 170
Db   111 TKLSIPTDSIWVPDILLINEFVDVGKSPNIPYVYVHHRGEVQNYKPLQLVTACSLDIYNFP 170

Qy   171 FDQQNCTTFSSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMG 230
Db   171 FDVQNCSLTFTSWLHTIQDINITLWRSPEVR-SDKSIFINQGEWELLEVFPQFQKEFSID 229

Qy   231 -NNLYDQIMFYVAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGY 289
Db   230 ISNSYAEMKFYVIIRRRPLFYAVSLLLPSIFLMVVDIVGFCLPPDSGERVSFKITLLLGY 289

Qy   290 SVFLIIVSDTLPATAIGTPLIGVYFVVCMALLVISLAETIFIVRLVHKQDLQ-RPVPDWL 347
Db   290 NVFLLMNDLLPAS--GTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWL 347

Qy   348 HSLLLH------C-TSPGRCCPTAPQKGNK-----GLGLTLTHLPGPKEPGEL---AGK 391
Db   348 RHLVLDRIAWILCLGEQPMAHRPPATFQANKTDDCSHVGGPQDLEKTPRGRGS 408

Qy   392 KLGPRETEPDGGSGWTKTQLMEL--------------WVQFSHAMDTLFLFRLYLL 432
Db   409 PLPP----PREASLAVRGLLQELSSIRHFLEKRDEMREVARDWLRVGYVLDRLLFRIYLL 464

Qy   433 FMASSILTVIVLWN 446
Db   465 AVLAYSITLVTLWS 478

RESULT 3
US-11-037-829A-7
; Sequence 7, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
;   APPLICANT: Targacept, Inc
;   APPLICANT: Catholic Healthcare West
;   APPLICANT: Bencherif, Merouane
;   APPLICANT: Lukas, Ronald J.
;   TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
;   TITLE OF INVENTION: Nicotinic Receptor Subunits
;   FILE REFERENCE: T103 1520.PCT
;   CURRENT APPLICATION NUMBER: US/11/037,829A
;   CURRENT FILING DATE: 2005-01-18
;   PRIOR APPLICATION NUMBER: US 60/397,380
;   PRIOR FILING DATE: 2002-07-19
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 495
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: human nAChR alpha4-mouse 5HT3-FLAG chimera
US-11-037-829A-7

Query Match   22.4%; Score 529; DB 7; Length 495;
Best Local Similarity   29.2%; Pred. No. 2.5e-42;
Matches 129; Conservative 85; Mismatches 164; Indels 64; Gaps 12;

Qy   55 RPFTNYSIPTRVNISFTLSAILGVDAQLQLLTSFLMDLVWDNPFINWNPKECVGINKLT 114
Db   53 RPVANISDVVLVRFGLSIAQLIDVDEKNQMMTTNVVKQEWHDYKLRWDPADYENVTSIR 112

Qy   115 VLAENLWLPDIFIVESMDVDQTPSGLT-AYISSEGRIKYDKPMRVTSICNLDIFYFPDQ 173
Db   113 IPSELIWRPDILVLNNADGDFAVTHLTKAHLFHDGRVQWTPPAIYKSSCSIIDVTFPFDQ 172

Qy   174 QNCTTFTSSFLYTVDSMLLGMDKEVWEITDTSRKVIQ----TQGEWELLGI--NKATPKM 227
Db   173 QNCTMKFGSWTY----------DKAKIDLVNMHSRVDQLDFWESGEWVIVDAVGTYNTRKY 223

Qy   228 SMGNNLYDQIMFYVAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLL 287
Db   224 ECCABIYPDITYAFVIRRLPLFYTINLLIIPCLLISCLTVLVFYLPSECGEKITLCISVLL 283

Qy   288 GYNVFLLMNDLLPASG--TPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPR 345
Db   284 SLTVFLLITEIIPSTSLVIPLIGVYFVVCMALLVISLAETIFIVRLVIHKQDLQ-RPVPD 342

Qy   346 WLHSLLLH------C-TSPGRCCPTAPQKGNK---------GLGLTLTHLPGPKEPG 386
Db   343 WLRHLVLDRIAWILCLGEQPMAHRPPATFQANKTDDCSGSDLLPAMGNHCSHVGGPQDLE 402

Qy   387 EL--AGKKLGPRETEPDGGSGWTKTQLMEL------------WVQFSHAMDT 424
Db   403 KTPRGRGSPLPP----PREASLAVRGLLQELSSIRHFLEKRDEMREVARDWLRVGYVLDR 458

Qy   425 LLFRLYLLFMASSILTVIVLWN 446
Db   459 LLFRIYLLAVLAYSITLVTLWS 480

RESULT 4
US-11-122-144-10
; Sequence 10, Application US/11122144
; Publication No. US20050287663A1
;   GENERAL INFORMATION:

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              GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on:     April 12, 2006, 09:05:33 ; Search time 234 Seconds
                                          (without alignments)
                                  1347.740 Million cell updates/sec

Title:        US-10-661-378-9
Perfect score: 2360
Sequence:     1 MEGGWPARQSALLCLTVSLL.........RLYLLFMASSILTVIVLWNT 447

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:     2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:       2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    UniProt_05.80:*
              1: uniprot_sprot:*
              2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2348	99.5	447	2	Q8WXA8_HUMAN	Q8wxa8 homo sapien
2	1777.5	75.3	471	2	Q7Z6B2_HUMAN	Q7z6b2 homo sapien
3	1745	73.3	441	2	Q6V707_HUMAN	Q6v707 homo sapien
4	1725	73.1	456	2	Q6V706_HUMAN	Q6v706 homo sapien
5	1191	50.5	454	2	Q70244_HUMAN	Q70244 homo sapien
6	778.5	33.0	279	2	Q7Z6B3_HUMAN	Q7z6b3 homo sapien
7	766	32.5	478	1	5HT3R_HUMAN	5HT3R_HUMAN
8	766	32.5	484	2	Q7KZM7_HUMAN	Q7kzm7 homo sapien
9	738.5	31.3	483	2	Q9N0F4_MUSPF	Q9n0f4 mustela put
10	738	31.3	490	1	5HT3R_CAVPO	5HT3R_CAVPO cavia porce
11	731.5	31.0	483	1	5HT3R_RAT	P35563 rattus norv
12	729.5	30.9	477	2	Q62999_RAT	Q62999 rattus norv
13	720	30.5	483	2	Q8K1F4_MOUSE	Q8k1f4 mus musculu
14	717.5	30.4	487	1	5HT3R_MOUSE	5HT3R_MOUSE mus musculu
15	714	30.3	483	2	Q6J1J7_MOUSE	Q6j1j7 mus musculu
16	628	26.6	457	2	Q4SRT3_TETNG	Q4srt3 tetraodon n
17	592	25.1	1044	2	Q4RU50_TETNG	Q4ru50 tetraodon n
18	574.5	24.3	459	2	Q7ZTN5_XENLA	Q7ztn5 xenopus lae
19	560	23.7	445	2	Q4SRT2_TETNG	Q4srt2 tetraodon n
20	539.5	22.9	437	2	Q9JHJ5_MOUSE	Q9jhj5 mus musculu
21	526.5	22.3	441	2	O95264_HUMAN	O95264 homo sapien
22	524.5	22.2	437	2	Q9JJ16_RAT	Q9jj16 rattus norv
23	515.5	21.8	228	2	Q4RU51_TETNG	Q4ru51 tetraodon n
24	450.5	19.1	464	1	ACHB3_MOUSE	Q8bmn3 mus musculu
25	446.5	18.9	464	1	ACHB3_RAT	ACHB3_RAT
26	439.5	18.6	452	1	ACH10_CHICK	P12391 rattus norv
27	439.5	18.6	464	2	Q6PW48_RAT	Q918c7 gallus gall
28	436.5	18.5	509	2	Q7T2R3_FUGRU	Q6pw48 rattus rat
29	436	18.5	475	2	Q4SPT0_TETNG	Q7t2r3 fugu rubrip
30	435	18.4	475	2	Q4S3I3_TETNG	Q4spt0 tetraodon n
31	435	18.4	528	1	ACHA2_CHICK	Q4s3i3 tetraodon n
32	434.5	18.4	465	2	Q6WBY6_FUGRU	Q6by6 fugu rubrip
33	431.5	18.3	503	2	Q4S3I4_TETNG	Q4s3i4 tetraodon n
34	428.5	18.2	479	1	ACHA9_HUMAN	Q9ugm1 homo sapien
35	428.5	18.2	479	2	Q4W5A2_HUMAN	Q4w5a2 homo sapien
36	426.5	18.1	476	2	Q68RJ6_ONCMY	Q68rj6 oncorhynchu
37	426.5	18.1	555	2	Q7T2U0_FUGRU	Q7t2u0 fugu rubrip
38	426	18.1	495	1	ACHA3_BOVIN	O07263 bos taurus
39	425.5	18.0	513	2	Q7T2R9_FUGRU	Q7t2r9 fugu rubrip
40	425	18.0	550	1	ACH92_ONCMY	Q68rj7 oncorhynchu
41	424.5	18.0	530	2	Q4TOS4_TETNG	Q4t0s4 tetraodon n
42	424.5	18.0	561	2	Q4RIC6_TETNG	Q4ric6 tetraodon n
43	423	17.9	499	1	ACHA3_MOUSE	Q8r4g9 mus musculu
44	423	17.9	499	2	Q8VHH6_MOUSE	Q8vhh6 mus musculu
45	423	17.9	622	2	Q7T2S3_FUGRU	Q7t2s3 fugu rubrip

ALIGNMENTS

```
RESULT 1
Q8WXA8_HUMAN
ID   Q8WXA8_HUMAN PRELIMINARY;      PRT;    447 AA.
AC   Q8WXA8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   5-hydroxytryptamine receptor 3 subunit C.
GN   Name=HTR3C;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Dubin A.E., Erlander M.G., Huvar A., Huvar R., Buehler L.K.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC       family.
DR   EMBL; AF459285; AAL66182.1; -; mRNA.
DR   HSSP; P02711; 1OED.
DR   Ensembl; ENSG00000178084; Homo sapiens.
DR   HGNC; HGNC:24003; HTR3C.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045211; C:postsynaptic membrane; IEA.
DR   GO; GO:0005230; F:extracellular ligand-gated ion channel acti...  .; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR006201; Neur_channel.
DR   InterPro; IPR006202; Neur_chan_LBD.
DR   InterPro; IPR006029; Neu_channel_memb.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW   Transmembrane; Transport.
SQ   SEQUENCE   447 AA;  50247 MW;  EA8146A2AAA2E1D7 CRC64;

Query Match             99.5%;  Score 2348;  DB 2;  Length 447;
Best Local Similarity   99.6%;  Pred. No. 1.3e-177;
Matches  445;  Conservative   0;  Mismatches   2;  Indels    0;  Gaps    0;

Qy    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEGGWPARQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKAFRPFTNY 60

Qy   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SIPTRVNISFTLSAILGVDAQLQLLTSFLWMDLVWDNPFINWNPKECVGINKLTVLAENL 120
```

RESULT 2

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Qy  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTF 180
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  121 WLPDIFIVESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICKLDIFYFPFDQQNCTFTF 180

Qy  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 SSFLYTVDSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFY 240

Qy  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGYNVFLLMMNDLL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VAIRRRPSLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGYNVFLLMMNDLL 300

Qy  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 PASGTPLISVYFALCLSLMVVSLLETVFITYLLHVATTQPPPMPRWLHSLLLHCTSPGRC 360

Qy  361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQLMELWVQFSH 420
        |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  361 CPTAPQKGNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSSAWTKTQLMELWVQFSH 420

Qy  421 AMDTLLFRLYLLFMASSILTVIVLWNT 447
        |||||||||||||||||||||||||||
Db  421 AMDTLLFRLYLLFMASSILTVIVLWNT 447
```

```
RESULT 2
Q7Z6B2_HUMAN
ID   Q7Z6B2_HUMAN PRELIMINARY;     PRT;   471 AA.
AC   Q7Z6B2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   5-hydroxytryptamine serotonin receptor 3E.
GN   Name=HTR3E;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22688529; PubMed=12801637; DOI=10.1016/S0378-1119(03)00503-1;
RA   Niesler B., Frank B., Kapeller J., Rappold G.A.;
RT   "Cloning, physical mapping and expression analysis of the human 5-
RT   HT(3) serotonin receptor-like genes HTR3C, HTR3D and HTR3E.";
RL   Gene 310:101-111(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC       family.
DR   EMBL; AY159813; AAO38167.1; -; mRNA.
DR   Ensembl; ENSG00000186038; Homo sapiens.
DR   HGNC; HGNC:24005; HTR3E.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045211; C:postsynaptic membrane; IEA.
DR   GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR006201; Neur_channel.
DR   InterPro; IPR006202; Neur_chan_LBD.
DR   InterPro; IPR006029; Neur_chan_memb.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR002252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR   PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN 1.
KW   Ion transport; Ionic channel; Postsynaptic membrane; Receptor;
KW   Transmembrane; Transport.
SQ   SEQUENCE   471 AA;   52870 MW;   E51343F693B02F5B CRC64;

Query Match   75.3%;  Score 1777.5;  DB 2;  Length 471;
```

```
Best Local Similarity  74.2%;  Pred. No. 2.3e-132;
Matches 333;  Conservative 44;  Mismatches 63;  Indels 9;  Gaps 1;

Qy    8 RQSALLCLTVSLLLQGRGDAFTINCSGFDQHGVDPAVFQAVFDRKARPFTNYSIPTRVN  67
         :|:||: |: ||| ||||||| || |::::| |:.| ::|::: ||: |:|:|
Db   23 RRVALLHLTHSMSTTGRGVFTTINCSGFGQHGADPTALNSVFNRKPFRPVTNISVLTQVN  82

Qy   68 ISFFLSAILGVDAQLQLLTSFLWMDLVWDNPPINWNPKECVGINKLTVLAENLWLPDIFI 127
        ||| :|||| |:.|| :||:|||::|:|||||:| ||||:|  ::|: :||:|||||||||
Db   83 ISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGITKMSMAAKNLWLPDIFI 142

Qy  128 VESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFPFDQQNCTFTFSSFLYTV 187
         | |||||:||.|||||:|:||||:|:||:|.|||||||||||||||||||.|||||||||
Db  143 IELMDVDKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFPFDQQNCTLTFSSFLYTV 202

Qy  188 DSMLLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSMGNNLYDQIMFYVAIRRRP 247
        |||| |:|||||||||:||::||||:|||||||.:|||:|  |||||| |:||||||||||
Db  203 DSMLLDMEKEVWEITDASRNLQTHGEWELLGLSKATAKLSRGGNLYDRIVFYVAIRRRP 262

Qy  248 SLYIINLLVPSSFLVAIDALSFYLPAESENRAPFKITLLLGYNVFLLMMNDLLPASGTPL 307
        ||||:|||||| ||||||||||||||:.:.||.||||||||||||||||.|||||:||||
Db  263 SLYIVNLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLLLGYNVFLLMMSDLLPTSGTPL 322

Qy  308 ISVYFALCLSLMVVSLLETVFITYLLHVATTQPPMPRWLHSLLLHCTSPGRCCPTAPQK 367
        |.||||||||||| ||||||:||| |||||||||| ||||||||||.|||||||||||||
Db  323 IGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLPRWLHSLLLHCNSPGRCCPTAPQK 382

Qy  368 GNKGLGLTLTHLPGPKEPGELAGKKLGPRETEPDGGSGWTKTQ------LMELWVQF 418
         ||| |||| |||| |||| |:| :.||| |:  ||  |  | |        ||:|:||
Db  383 ENKGPGLTPTHLPGVKEPBVSAGQMPGPAEAELTGGSEWTRAQREHEAQKQHSVELWLQF 442

Qy  419 SHAMDTLLFRLYLLFMASSILTVIVLWNT 447
        ||||| :||||||||||||||:||:.|||
Db  443 SHAMDAMLFRLYLLFMASSITVICLWNT 471
```

```
RESULT 3
Q6V707_HUMAN
ID   Q6V707_HUMAN PRELIMINARY;     PRT;   441 AA.
AC   Q6V707;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   5-HT3c1 serotonin receptor-like protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22959642; PubMed=14597179; DOI=10.1016/S0378-1119(03)00803-5;
RA   Karnovsky A.M., Gotow L.F., McKinley D.D., Piechan J.L., Ruble C.L.,
RA   Mills C.J., Schellin K.A., Slightom J.L., Fitzgerald L.R.,
RA   Benjamin C.W., Roberds S.L.;
RT   "A cluster of novel serotonin receptor 3-like genes on human
RT   chromosome 3.";
RL   Gene 319:137-148(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)
CC       family.
DR   EMBL; AY349352; AAQ93476.1; -; mRNA.
DR   Ensembl; ENSG00000186038; Homo sapiens.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045211; C:postsynaptic membrane; IEA.
DR   GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR006201; Neur_channel.
DR   InterPro; IPR006202; Neur_chan_LBD.
DR   InterPro; IPR006029; Neu_Channel_memb.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
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